

<!--StartFragment-->RESULT 4

AAAY82326

ID AAY82326 standard; protein; 357 AA.

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AC AAY82326;

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DT 21-JUN-2000 (first entry)

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DE Human arginase I SEQ ID NO:17.

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KW Human; arginase II; arginase I; diagnosis; hypotensive; hypertensive;

KW uropathic; cytostatic; neuroprotective; gene therapy; hypertension;

KW nitric oxide biosynthesis modulator; urea cycle disease; hypotension;

KW episodic hyperammonaemia; hyperargininaemia; spasticity; prostatitis;

KW growth retardation; progressive mental impairment; prostate disease;

KW prostate cancer; benign prostatic hyperplasia; hypertrophy;

KW prostate damage; kidney disease; kidney damage.

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OS Homo sapiens.

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PN US6054308-A.

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PD 25-APR-2000.

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PF 15-JUL-1998; 98US-00116115.

XX

PR 14-MAR-1996; 96US-0013395P.

PR 20-AUG-1996; 96US-00700186.

PR 20-AUG-1997; 97US-00914981.

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PA (HUMA-) HUMAN GENOME SCI INC.

PA (SMIK) SMITHKLINE BEECHAM CORP.

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PI Dillon PJ, Vockley JG;

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DR WPI; 2000-328355/28.

DR N-PSDB; AAA08074.

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PT Novel human arginase II polypeptides useful for treating urea cycle

PT diseases, hypertension, hypotension, episodic hyperammonemia, to control

PT nitric oxide formation and kidney damage.

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PS Example 1; Col 49-52; 37pp; English.

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CC The present invention describes human arginase II. Arginase II has

CC hypotensive, hypertensive, uropathic, cytostatic and neuroprotective

CC activities, and can be used in gene therapy and as a nitric oxide

CC biosynthesis modulator. Human arginase II proteins can be used to treat

CC diseases associated with or caused by a defect in the arginase II gene or

Qy	1	MSAKSRTIGIIGAPFSKGQPRGGVEEGPTVLRKAGLLEKLKEQECVDVKDYGDLPFADIPN	60
Db	18	MSAKSRTIGIIGAPFSKGQPRGGVEEGPTVLRKAGLLEKLKEQECVDVKDYGDLPFADIPN	77
Qy	61	DSPFQIVKNPRSVGKASEQLAGKVAQVKKNGRISLVLGGDHSLAIGSISGHARVHPDLGV	120
Db	78	DSPFQIVKNPRSVGKASEQLAGKVAQVKKNGRISLVLGGDHSLAIGSISGHARVHPDLGV	137
Qy	121	IWVDAHTDINTPLTTTSGNLHGQPVSFLLKELKGKIPDVPGFSWVTPCISAKDIVYIGLR	180
Db	138	IWVDAHTDINTPLTTTSGNLHGQPVSFLLKELKGKIPDVPGFSWVTPCISAKDIVYIGLR	197
Qy	181	DVDPGEHYILKTLGIIKYFSMTEVDRLGIGKVMEEETLSYLLGRKKRPIHLSFDVDGLDPSF	240
Db	198	DVDPGEHYILKTLGIIKYFSMTEVDRLGIGKVMEEETLSYLLGRKKRPIHLSFDVDGLDPSF	257
Qy	241	TPATGTPVVGGLTYREGLYITEEIYKTGLLSGLDIMEVNPSLGKTPEEVTRTVNTAVAIT	300
Db	258	TPATGTPVVGGLTYREGLYITEEIYKTGLLSGLDIMEVNPSLGKTPEEVTRTVNTAVAIT	317
Qy	301	LACFGLAREGNHKPIDYLNPPK	322
Db	318	LACFGLAREGNHKPIDYLNPPK	339

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